

4040.001000  
SEQUENCE LISTING

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<120> Modification of Feeding Behavior Using PYY and GLP-1

<130> 4040.001000

<150> PCT/GB03/00062  
<151> 2003-01-10

<150> PCT/US02/31944  
<151> 2002-09-24

<150> 60/392,109  
<151> 2002-06-28

<150> GB 0200507.2  
<151> 2002-01-10

<160> 341

<170> PatentIn version 3.1

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<213> Homo sapiens

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Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu  
1 5 10 15  
Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr  
20 25 30  
Arg Gln Arg Tyr  
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<212> PRT  
<213> Homo sapiens

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Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp  
1 5 10 15  
Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30

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Arg Gln Arg Tyr  
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<210> 3  
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Ala Ser Leu Glu Pro Glu Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln  
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr  
20 25 30

Arg Pro Arg Tyr  
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<210> 4  
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<400> 4

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Tyr Pro Ala Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu  
1 5 10 15

Leu Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr  
20 25 30

Arg Gln Arg Tyr  
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<210> 6  
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<213> Sus sp.

<400> 6

Tyr Pro Ala Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu  
1 5 10 15

Leu Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr  
20 25 30

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Arg Gln Arg Tyr  
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<210> 7  
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<213> *Cavia porcellus*

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Tyr Pro Ser Lys Pro Glu Ala Pro Gly Ser Asp Ala Ser Pro Glu Glu  
1 5 10 15

Leu Ala Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr  
20 25 30

Arg Gln Arg Tyr  
35

<210> 8  
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<213> *Rana sp.*

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Tyr Pro Pro Lys Pro Glu Asn Pro Gly Glu Asp Ala Ser Pro Glu Glu  
1 5 10 15

Met Thr Lys Tyr Leu Thr Ala Leu Arg His Tyr Ile Asn Leu Val Thr  
20 25 30

Arg Gln Arg Tyr  
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<212> PRT  
<213> *Raja sp.*

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Tyr Pro Pro Lys Pro Glu Asn Pro Gly Asp Asp Ala Ala Pro Glu Glu  
1 5 10 15

Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30

Arg Gln Arg Tyr  
35

<210> 10  
<211> 36  
<212> PRT  
<213> *Dogfish sp.*

<400> 10

Tyr Pro Pro Lys Pro Glu Asn Pro Gly Glu Asp Ala Pro Pro Glu Glu  
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1                      5                      10                      15  
 Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
                     20                      25                      30  
 Arg Gln Arg Tyr  
                     35

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Phe Pro Pro Lys Pro Asp Asn Pro Gly Asp Asn Ala Ser Pro Glu Gln  
 1                      5                      10                      15  
 Met Ala Arg Tyr Lys Ala Ala Val Arg His Tyr Ile Asn Leu Ile Thr  
                     20                      25                      30  
 Arg Gln Arg Tyr  
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Met Pro Pro Lys Pro Asp Asn Pro Ser Pro Asp Ala Ser Pro Glu Glu  
 1                      5                      10                      15  
 Leu Ser Lys Tyr Met Leu Ala Val Arg Asn Tyr Ile Asn Leu Ile Thr  
                     20                      25                      30  
 Arg Gln Arg Tyr  
                     35

<210> 13  
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Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp  
 1                      5                      10                      15  
 Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
                     20                      25                      30  
 Arg Gln Arg Tyr  
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<213> Oryctolagus cuniculus

<400> 14

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp  
1 5 10 15  
Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30  
Arg Gln Arg Tyr  
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<210> 15

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<212> PRT

<213> Canis familiaris

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Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp  
1 5 10 15  
Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30  
Arg Gln Arg Tyr  
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<210> 16

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<212> PRT

<213> Sus sp.

<400> 16

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp  
1 5 10 15  
Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30  
Arg Gln Arg Tyr  
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<210> 17

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<212> PRT

<213> Bos taurus

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Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp  
1 5 10 15  
Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30  
Arg Gln Arg Tyr  
35

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<400> 18

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Asp Asp Ala Pro Ala Glu Asp  
1 5 10 15

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30

Arg Gln Arg Tyr  
35

<210> 19  
<211> 36  
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<213> Cavia porcellus

<400> 19

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp  
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Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30

Arg Gln Arg Tyr  
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<210> 20  
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<400> 20

Tyr Pro Ser Lys Pro Asp Ser Pro Gly Glu Asp Ala Pro Ala Glu Asp  
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30

Arg Gln Arg Tyr  
35

<210> 21  
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<400> 21

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp  
1 5 10 15

Met Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
Page 6

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20

25

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Arg Gln Arg Tyr  
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<210> 22  
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<212> PRT  
<213> Carassius auratus

<400> 22

Tyr Pro Thr Lys Pro Asp Asn Pro Gly Glu Gly Ala Pro Ala Glu Glu  
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Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30

Arg Gln Arg Tyr  
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<210> 23  
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<400> 23

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Gly Ala Pro Ala Glu Asp  
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Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30

Arg Gln Arg Tyr  
35

<210> 24  
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<400> 24

Pro Pro Asn Lys Pro Asp Ser Pro Gly Glu Asp Ala Pro Ala Glu Asp  
1 5 10 15

Leu Ala Arg Tyr Leu Ser Ala Val Arg His Tyr Ile Asn Leu Ile Thr  
20 25 30

Arg Gln Arg Tyr  
35

<210> 25  
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<213> Ovis aries

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Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln  
1 5 10 15

Met Ala Gln Tyr Ala Ala Asp Leu Arg Arg Tyr Ile Asn Met Leu Thr  
20 25 30

Arg Pro Arg Tyr  
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<213> Sus sp.

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Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asp Ala Thr Pro Glu Gln  
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Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr  
20 25 30

Arg Pro Arg Tyr  
35

<210> 27  
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<212> PRT  
<213> Canis familiaris

<400> 27

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asp Ala Thr Pro Glu Gln  
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Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr  
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Arg Pro Arg Tyr  
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<213> Felis catus

<400> 28

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln  
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Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr  
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Arg Pro Arg Tyr  
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Ala Pro Leu Glu Pro Glu Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln  
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Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr  
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Arg Pro Arg Tyr  
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Ala Pro Leu Glu Pro Met Tyr Pro Gly Asp Tyr Ala Thr His Glu Gln  
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Arg Ala Gln Tyr Glu Thr Gln Leu Arg Arg Tyr Ile Asn Thr Leu Thr  
20 25 30

Arg Pro Arg Tyr  
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<210> 31  
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<213> Mus musculus

<400> 31

Ala Pro Leu Glu Pro Met Tyr Pro Gly Asp Tyr Ala Thr Pro Glu Gln  
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Met Ala Gln Tyr Glu Thr Gln Leu Arg Arg Tyr Ile Asn Thr Leu Thr  
20 25 30

Arg Pro Arg Tyr  
35

<210> 32  
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Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln  
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Gln Met Ala Gln Tyr Ala Ala Glu Met Arg Arg Tyr Ile Asn Met Leu  
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Thr Arg Pro Arg Tyr  
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Gly Pro Ser Gln Pro Thr Tyr Pro Gly Asp Asp Ala Pro Val Glu Asp  
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Leu Ile Arg Phe Tyr Asn Asp Leu Gln Gln Tyr Leu Asn Val Val Thr  
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Arg His Arg Tyr  
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<210> 34  
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<213> Alligator sp.

<400> 34

Thr Pro Leu Gln Pro Lys Tyr Pro Gly Asp Gly Ala Pro Val Glu Asp  
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Leu Ile Gln Phe Tyr Asn Asp Leu Gln Gln Tyr Leu Asn Val Val Thr  
20 25 30

Arg Pro Arg Phe  
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<210> 35  
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<213> Rana catesbeiana

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Ala Pro Ser Glu Pro His His Pro Gly Asp Gln Ala Thr Pro Asp Gln  
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Leu Ala Gln Tyr Tyr Ser Asp Leu Tyr Gln Tyr Ile Thr Phe Ile Thr  
20 25 30

Arg Pro Arg Phe  
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Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Arg His Thr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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<400> 38

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Arg His Tyr Ile Asn Leu Val Thr Arg Gln Arg Tyr  
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Arg His Tyr Val Asn Leu Val Thr Arg Gln Arg Tyr  
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Arg His Tyr Leu Gln Leu Val Thr Arg Gln Arg Tyr  
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<400> 42  
Arg His Tyr Leu Asn Ile Val Thr Arg Gln Arg Tyr  
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<400> 43  
Arg His Tyr Leu Asn Val Val Thr Arg Gln Arg Tyr  
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<210> 44  
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<400> 44  
Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Tyr  
1 5 10

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Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr  
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<400> 46

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Arg Tyr  
1 5 10

<210> 47  
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<400> 47

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Arg Tyr  
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<400> 48

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Arg Tyr  
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Arg His Tyr Leu Asn Leu Val Thr Arg Gln Lys Tyr  
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Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Thr  
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<400> 51

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Phe  
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<400> 52

Lys His Thr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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<400> 53

Lys His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Lys His Tyr Ile Asn Leu Val Thr Arg Gln Arg Tyr  
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Lys His Tyr Val Asn Leu Val Thr Arg Gln Arg Tyr  
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<400> 56

Lys His Tyr Leu Gln Leu Val Thr Arg Gln Arg Tyr  
1 5 10

<210> 57  
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<400> 57

Lys His Tyr Leu Asn Ile Val Thr Arg Gln Arg Tyr  
1 5 10

<210> 58  
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Lys His Tyr Leu Asn Val Val Thr Arg Gln Arg Tyr  
1 5 10

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Lys His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Tyr  
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Lys His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr  
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Lys His Tyr Leu Asn Leu Val Ser Arg Gln Arg Tyr  
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Lys His Tyr Leu Asn Leu Val Thr Lys Gln Arg Tyr  
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Lys His Tyr Leu Asn Leu Val Thr Arg Asn Arg Tyr  
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Lys His Tyr Leu Asn Leu Val Thr Arg Gln Lys Tyr  
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Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Thr  
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Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Phe  
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Arg His Thr Ile Asn Leu Val Thr Arg Gln Arg Tyr  
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Arg His Thr Val Asn Leu Val Thr Arg Gln Arg Tyr  
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Arg His Thr Leu Gln Leu Val Thr Arg Gln Arg Tyr  
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Arg His Thr Leu Asn Ile Val Thr Arg Gln Arg Tyr  
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Arg His Thr Leu Asn Val Val Thr Arg Gln Arg Tyr  
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Arg His Thr Leu Asn Leu Ile Thr Arg Gln Arg Tyr  
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Arg His Thr Leu Asn Leu Leu Thr Arg Gln Arg Tyr  
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Arg His Thr Leu Asn Leu Val Ser Arg Gln Arg Tyr  
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Arg His Thr Leu Asn Leu Val Thr Lys Gln Arg Tyr  
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Arg His Thr Leu Asn Leu Val Thr Arg Asn Arg Tyr  
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Arg His Thr Leu Asn Leu Val Thr Arg Gln Lys Tyr  
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Arg His Thr Leu Asn Leu Val Thr Arg Gln Arg Thr  
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Arg His Thr Leu Asn Leu Val Thr Arg Gln Arg Phe  
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Arg His Phe Ile Asn Leu Val Thr Arg Gln Arg Tyr  
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Arg His Phe Val Asn Leu Val Thr Arg Gln Arg Tyr  
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Arg His Phe Leu Gln Leu Val Thr Arg Gln Arg Tyr  
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Arg His Phe Leu Asn Ile Val Thr Arg Gln Arg Tyr  
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Arg His Phe Leu Asn Val Val Thr Arg Gln Arg Tyr  
1 5 10

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Arg His Phe Leu Asn Leu Ile Thr Arg Gln Arg Tyr  
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Arg His Phe Leu Asn Leu Leu Thr Arg Gln Arg Tyr  
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Arg His Phe Leu Asn Leu Val Ser Arg Gln Arg Tyr  
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Arg His Phe Leu Asn Leu Val Thr Lys Gln Arg Tyr  
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Arg His Phe Leu Asn Leu Val Thr Arg Asn Arg Tyr  
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Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Thr Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Ser Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Phe Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg  
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Tyr

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Thr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg  
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Tyr

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Phe Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg  
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Tyr

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Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln  
1 5 10 15

Arg Tyr

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Lys Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln  
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Arg Tyr

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Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg  
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Gln Arg Tyr

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Gln Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg  
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Gln Arg Tyr

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Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr  
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Arg Gln Arg Tyr  
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Ile Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr  
1 5 10 15

Arg Gln Arg Tyr  
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Val Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr  
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Arg Gln Arg Tyr  
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<400> 165

Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val  
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Thr Arg Gln Arg Tyr  
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Asp Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val  
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Thr Arg Gln Arg Tyr  
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Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu  
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Val Thr Arg Gln Arg Tyr  
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<400> 168

Asp Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu  
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Val Thr Arg Gln Arg Tyr  
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<400> 169

Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn  
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Leu Val Thr Arg Gln Arg Tyr  
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Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu  
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Asn Leu Val Thr Arg Gln Arg Tyr  
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Thr Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu  
1 5 10 15

Asn Leu Val Thr Arg Gln Arg Tyr  
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Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr  
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Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Ser Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr  
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Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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<400> 174

Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His  
1 5 10 15  
Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
20 25

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<400> 175

Glu Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His  
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Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
20 25

<210> 176  
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<400> 176

Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg  
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His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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<400> 177

Asp Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg  
1 5 10 15

His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
20 25

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<400> 178

Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu  
1 5 10 15

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
20 25

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<400> 179

Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser  
1 5 10 15

Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
20 25

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Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala  
1 5 10 15

Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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<211> 30

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<400> 181

Ser Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala  
1 5 10 15

Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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<210> 182

<211> 31

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<400> 182

Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr  
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Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
20 25 30

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<211> 31

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<400> 183

Asp Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr  
1 5 10 15

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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<400> 184

Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr  
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Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
20 25 30

<210> 185

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<400> 185

Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg  
1 5 10 15  
Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg  
20 25 30

Tyr

<210> 186

<211> 33

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<400> 186

Arg Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg  
1 5 10 15  
Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg  
20 25 30

Tyr

<210> 187

<211> 33

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Gln Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg  
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Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg  
20 25 30

Tyr

<210> 188  
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Asn Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg  
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Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg  
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Tyr

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<400> 189

Leu Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn  
1 5 10 15

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln  
20 25 30

Arg Tyr

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<400> 190

Val Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn  
1 5 10 15

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln  
20 25 30

Arg Tyr

<210> 191  
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Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
 1 5 10 15

<210> 194  
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Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
 1 5 10 15

<210> 195  
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Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg  
1 5 10 15

Tyr

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<400> 196

Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln  
1 5 10 15

Arg Tyr

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Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg  
1 5 10 15

Gln Arg Tyr

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<400> 198

Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr  
1 5 10 15

Arg Gln Arg Tyr  
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<210> 199



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<400> 199

Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val  
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Thr Arg Gln Arg Tyr  
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<400> 200

Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu  
1 5 10 15

Val Thr Arg Gln Arg Tyr  
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<210> 201  
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<400> 201

Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn  
1 5 10 15

Leu Val Thr Arg Gln Arg Tyr  
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<400> 202

Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn  
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Leu Val Thr Arg Gln Arg Tyr  
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<400> 203

Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu  
1 5 10 15

Asn Leu Val Thr Arg Gln Arg Tyr  
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Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr  
1 5 10 15

Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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<400> 205

Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His  
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Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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<400> 206

Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu  
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Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser  
1 5 10 15

Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser  
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Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala  
1 5 10 15

Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr  
1 5 10 15

Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
20 25 30

<210> 211

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<400> 211

Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr  
1 5 10 15

Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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<210> 212

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<400> 212

Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg  
1 5 10 15

Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg  
20 25 30

Tyr

<210> 213

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Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr  
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Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr  
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<400> 215

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr  
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Pro Ala Glu Asp Leu Ala Gln Tyr Ala Ala Glu Leu Arg His Tyr Leu  
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Asn Leu Leu Thr Arg Gln Arg Tyr  
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Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
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Arg Gln Arg Tyr  
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Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
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Arg Gln Arg Tyr  
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Ala Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr Arg  
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Gln Arg Tyr

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Arg Gln Arg Tyr  
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<223> AMIDATION

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Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln  
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Arg Tyr

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Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
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Arg Gln Arg Tyr  
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Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg  
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Gln Arg Tyr

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Ala Ala Arg Tyr Ser His Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
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Arg Gln Arg Tyr  
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Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg  
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Gln Arg Tyr

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Arg Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
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Arg Gln Arg Tyr  
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Gln Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln  
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Arg Tyr

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Ala Arg Phe Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg  
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Gln Arg Tyr

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Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
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Arg Gln Arg Tyr  
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Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
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Arg Gln Arg Tyr  
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Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
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Arg Gln Arg Tyr  
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Ala Arg Tyr Tyr Ser Glu Leu Arg Arg Tyr Ile Asn Leu Ile Thr Arg  
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Gln Arg Tyr

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Arg Gln Arg Tyr  
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Ala Arg Tyr Tyr Thr Gln Leu Arg His Tyr Ile Asn Leu Ile Thr Arg  
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Gln Arg Tyr

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Leu Ala Arg Tyr Tyr Ser Asn Leu Arg His Tyr Ile Asn Val Ile Thr  
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Arg Gln Arg Tyr  
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Ala Arg Tyr Tyr Asp Ser Leu Arg His Tyr Ile Asn Thr Ile Thr Arg  
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Gln Arg Tyr

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Ala Arg Tyr Tyr Ser Ala Leu Gln His Tyr Ile Asn Leu Leu Thr Arg  
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Arg Gln Arg Phe  
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Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln  
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Arg Phe

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Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg  
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Gln Arg Tyr

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Ser Arg Tyr Tyr Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg  
1 5 10 15



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Gln Arg Tyr

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Xaa Ala Arg Tyr Tyr Asn Ala Leu Arg His Phe Ile Asn Leu Ile Thr  
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Arg Gln Arg Tyr  
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Xaa Arg Tyr Glu Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg  
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His Arg Tyr

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Xaa Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile  
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Thr Arg Pro Arg Phe  
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Ala Leu Tyr Tyr Ser Ala Leu Arg His Phe Val Asn Leu Ile Thr Arg  
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Gln Arg Tyr

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Gln Arg Tyr

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<220>  
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<222> (1)..(1)  
<223> N terminus is bonded to H

<220>  
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<223> MeSer

<220>  
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<222> (18)..(18)  
<223> AMIDATION

<400> 247

Xaa Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Met Ile Thr Arg Gln  
1 5 10 15

Arg Phe

<210> 248  
<211> 20  
<212> PRT  
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<220>  
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<220>  
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<223> N terminus is bonded to H

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<222> (20)..(20)  
<223> AMIDATION

<400> 248

Arg Ile Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr  
1 5 10 15  
Arg Gln Arg Phe  
20

<210> 249  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<223> N terminal is bonded to H

<220>  
<221> MOD\_RES  
<222> (20)..(20)  
<223> AMIDATION

<400> 249

Leu Ser Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr  
1 5 10 15  
Arg Gln Arg Tyr  
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<210> 250  
<211> 19  
<212> PRT  
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<220>  
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<220>  
<221> MOD\_RES  
<222> (19)..(19)  
<223> AMIDATION

<220>  
<221> MISC\_FEATURE  
<222> (1)..(1)  
<223> Xaa is MeIle

<400> 250

Xaa Arg Tyr Tyr Ser Ala Leu Gln His Phe Ile Asn Leu Ile Thr Arg  
1 5 10 15

Gln Arg Tyr

<210> 251  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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 <223> D Ser

<220>  
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 <222> (1)..(1)  
 <223> N terminus is bonded to H

<220>  
 <221> MOD\_RES  
 <222> (19)..(19)  
 <223> AMIDATION

&lt;400&gt; 251

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg  
 1 5 10 15

Gln Arg Phe

<210> 252  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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 <223> N terminus is bonded to H

<220>  
 <221> MOD\_RES  
 <222> (20)..(20)  
 <223> AMIDATION

&lt;400&gt; 252

Met Ala Arg Tyr Tyr Ser Asp Leu Arg Arg Tyr Ile Asn Leu Ile Thr  
 1 5 10 15

Arg Gln Arg Tyr  
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&lt;210&gt; 253

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<211> 19  
<212> PRT  
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<220>  
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<223> N terminus is bonded to H

<220>  
<221> MOD\_RES  
<222> (19)..(19)  
<223> AMIDATION

<400> 253

Ala Arg Tyr Tyr Ser Glu Leu Arg His Tyr Ile Ile Leu Ile Thr Arg  
1 5 10 15

Gln Arg Tyr

<210> 254  
<211> 20  
<212> PRT  
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<220>  
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<220>  
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<222> (1)..(1)  
<223> D Ala

<220>  
<221> MOD\_RES  
<222> (20)..(20)  
<223> AMIDATION

<400> 254

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr  
1 5 10 15

Arg Gln Arg Tyr  
20

<210> 255  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<400> 255

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr  
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1

5

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15

<210> 256  
<211> 35  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
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<222> (25)..(25)  
<223> im DNP HIS; 2,2 diphenylalanine Hisitidine

<220>  
<221> MOD\_RES  
<222> (35)..(35)  
<223> AMIDATION

<400> 256

Tyr Pro Ala Lys Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu  
1 5 10 15

Ser Thr Tyr Tyr Ala Ser Leu Arg Xaa Tyr Leu Asn Leu Val Thr Arg  
20 25 30

Glx Arg Tyr  
35

<210> 257  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 257

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 258  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
<221> MOD\_RES  
<222> (15)..(15)

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<223> AMIDATION

<400> 258

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Ala Arg Gln Arg Tyr  
1 5 10 15

<210> 259

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide variation

<220>

<221> MOD\_RES

<222> (15)..(15)

<223> AMIDATION

<400> 259

Ala Ala Leu Arg His Tyr Leu Asn Leu Val Ala Arg Gln Arg Tyr  
1 5 10 15

<210> 260

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide variation

<220>

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<223> AMIDATION

<400> 260

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 261

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide variation

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> N alpha ACETYLATION

<220>

<221> MISC\_FEATURE

<222> (13)..(13)

<223> Xaa is Ornithine



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<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 261

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Xaa Arg Tyr  
1 5 10 15

<210> 262  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> Xaa is p.Cl.Pro; 4 chlorophenylalanine

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 262

Ala Ser Leu Arg Xaa Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 263  
<211> 15  
<212> PRT  
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<220>  
<223> Polypeptide variation

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 263

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

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<210> 264  
<211> 15  
<212> PRT  
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<220>  
<223> Polypeptide variation

<220>  
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<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<220>  
<221> MISC\_FEATURE  
<222> (15)..(15)  
<223> Xaa is N Me Tyr

<400> 264

Ala Ser Leu Arg His Phe Glu Asn Leu Val Thr Arg Gln Arg Xaa  
1 5 10 15

<210> 265  
<211> 15  
<212> PRT  
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<220>  
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<222> (13)..(13)  
<223> Xaa is Ornithine

<220>  
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<222> (1)..(1)  
<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<220>  
<221> MISC\_FEATURE  
<222> (15)..(15)  
<223> Xaa is N Me Tyr

<400> 265

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Xaa Arg Xaa  
1 5 10 15

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<210> 266  
<211> 15  
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<220>  
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<220>  
<221> LIPID  
<222> (1)..(1)  
<223> N alpha myristoyl

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 266

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 267  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
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<223> N alpha naphthateneacetyl

<220>  
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<400> 267

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 268  
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<213> Artificial Sequence

<220>  
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<220>  
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<223> Xaa is N Me Tyr

<220>

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<223> N alpha ACETYLATION

<220>  
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<223> AMIDATION

<220>  
<221> MISC\_FEATURE  
<222> (13)..(13)  
<223> Xaa is Ornithine

<400> 268

Ala Ser Leu Arg His Phe Glu Asn Leu Val Thr Arg Xaa Arg Xaa  
1 5 10 15

<210> 269  
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<220>  
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<220>  
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<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 269

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 270  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
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<222> (6)..(6)  
<223> Xaa is 3 benzothienylalanine

<220>  
<221> MOD\_RES  
<222> (7)..(7)  
<223> N alpha ACETYLATION

<220>

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<221> MOD\_RES  
<222> (1)..(1)  
<223> N alpha ACETYLATION

<400> 270

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 271  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
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<223> Xaa is 4,4' biphenylalanine

<220>  
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<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
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<400> 271

Xaa Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 272  
<211> 15  
<212> PRT  
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<220>  
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<220>  
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<223> N alpha ACETYLATION

<220>  
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<222> (15)..(15)  
<223> AMIDATION

<220>  
<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> Xaa is 3 benzothienylalanine

<400> 272

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Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 273  
<211> 15  
<212> PRT  
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<220>  
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<223> AMIDATION

<220>  
<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> Xaa is 3 benzothienalanine

<400> 273

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 274  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
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<222> (1)..(1)  
<223> N alpha ACETYLTATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 274

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 275  
<211> 15  
<212> PRT  
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<220>  
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<220>  
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<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 275

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 276  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<222> (15)..(15)  
<223> AMIDATION

<220>  
<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> Xaa is 2 thienylalanine

<400> 276

Ala Ser Leu Arg Asn Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 277  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<221> MOD\_RES  
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<223> AMIDATION

<220>  
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<222> (6)..(6)  
<223> Xaa is tetrahydroisoquinoline

<400> 277

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 278  
<211> 3  
<212> PRT  
<213> Homo sapiens

<400> 278

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<210> 279  
<211> 11  
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<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
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<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
<222> (11)..(11)  
<223> AMIDATION

<400> 279

His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10

<210> 280  
<211> 15  
<212> PRT  
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<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION



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<222> (1)..(1)  
<223> ACETYLATION

<220>  
<221> MISC\_FEATURE  
<222> (15)..(15)  
<223> Xaa is 2 thienylalanine

<400> 280

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Xaa  
1 5 10 15

<210> 281  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
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<222> (16)..(16)  
<223> AMIDATION

<220>  
<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> Xaa is 4 Thiazolylalanine

<400> 281

Ala Ser Leu Arg His Xaa Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 282  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
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<223> AMIDATION

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<220>  
<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> Xaa is 4 Thiazolylalanine

<400> 282

Ala Ser Leu Arg His Xaa Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 283  
<211> 3  
<212> PRT  
<213> Homo sapiens

<400> 283

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<210> 284  
<211> 3  
<212> PRT  
<213> Homo sapiens

<400> 284

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<400> 285

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<400> 286

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<400> 287

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<210> 288  
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<210> 289  
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<220>  
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<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 289

Phe Ser Leu Arg Asn Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 290  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> N alpha ACETYLTATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 290

Tyr Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

4040.001000

<210> 291  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> N alpha ACETYLTATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 291

Ala Ser Leu Arg His Tyr Trp Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 292  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> N alpha ACETYLTATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 292

Ala Ser Leu Arg His Tyr Leu Asn Trp Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 293  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
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<222> (1)..(1)  
<223> N alpha ACETYLTATION

<220>  
<221> MOD\_RES

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<222> (15)..(15)  
<223> AMIDATION

<400> 293

Ala Ser Leu Arg Ala Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 294  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
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<222> (1)..(1)  
<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
<222> (14)..(14)  
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<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> Xaa is 3' benzothienyalanine

<400> 294

Ala Ser Leu Arg Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10

<210> 295  
<211> 15  
<212> PRT  
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<220>  
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<220>  
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<220>  
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<223> AMIDATION

<400> 295

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 296

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<211> 15  
<212> PRT  
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<220>  
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<220>  
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<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 296

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Phe  
1 5 10 15

<210> 297  
<211> 15  
<212> PRT  
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<220>  
<223> Polypeptide variation

<220>  
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<222> (11)..(11)  
<223> Xaa is D form of Trp

<220>  
<221> MOD\_RES  
<222> (11)..(11)  
<223> AMIDATION

<220>  
<221> MOD\_RES  
<222> (11)..(11)  
<223> N alpha ACETYLATION

<400> 297

Ala Ser Leu Arg His Phe Leu Asn Leu Val Xaa Arg Gln Arg Tyr  
1 5 10 15

<210> 298  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<223> AMIDATION

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<221> MISC\_FEATURE

<222> (1)..(1)

<223> N terminus is bonded to CH3CO

<400> 298

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr  
1 5 10

<210> 299

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide variation

<220>

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<222> (13)..(13)

<223> AMIDATION

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<221> MISC\_FEATURE

<222> (1)..(1)

<223> N terminus is bonded to CH3CO

<400> 299

Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr  
1 5 10

<210> 300

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide variation

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> AMIDATION

<220>

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<222> (13)..(13)

<223> AMIDATION

<400> 300

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr  
1 5 10

<210> 301

<211> 13

4040.001000

<212> PRT  
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<220>  
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<223> AMIDATION

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<400> 301

Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr  
1 5 10

<210> 302  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
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<222> (1)..(1)  
<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<220>  
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<222> (15)..(15)  
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>  
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<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>  
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<223> Xaa is Norvaline

<220>  
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<222> (3)..(3)  
<223> Xaa is Norleucine

<220>  
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<222> (7)..(7)



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<223> Xaa is Norleucine

<220>

<221> MISC\_FEATURE

<222> (9)..(9)

<223> Xaa is Norleucine

<400> 302

Ala Ser Xaa Arg His Trp Xaa Asn Xaa Xaa Thr Arg Gln Xaa Xaa  
1 5 10 15

<210> 303

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Polypeptide variation

<220>

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<223> N alpha ACETYLATION

<220>

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<223> AMIDATION

<220>

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<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>

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<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>

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<223> Xaa is Norleucine

<220>

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<223> Xaa is Norleucine

<220>

<221> MISC\_FEATURE

<222> (10)..(10)

<223> Xaa is Norvaline

<400> 303

Ala Ser Xaa Arg His Trp Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa  
1 5 10 15

<210> 304

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<211> 15  
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<223> Xaa is Norvaline

<400> 304

Ala Ser Xaa Arg His Phe Xaa Asn Xaa Xaa Thr Arg Gln Xaa Xaa  
1 5 10 15

<210> 305  
<211> 15  
<212> PRT  
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<220>  
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<220>  
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<220>  
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<400> 305

Ala Ser Xaa Arg His Phe Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa  
1 5 10 15

<210> 306  
<211> 12  
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<220>

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<400> 306

Arg His Tyr Leu Asn Trp Val Thr Arg Gln Xaa Xaa  
1 5 10

<210> 307  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
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<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
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<223> AMIDATION

<400> 307

Arg His Tyr Leu Asn Trp Val Thr Arg Gln Arg Tyr  
1 5 10

<210> 308  
<211> 15  
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<220>  
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<223> AMIDATION

<220>  
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<220>  
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<223> Xaa is a psuedopeptide bond consisting of CH2 NH2

<220>

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<222> (10)..(10)  
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<400> 308

Ala Ser Leu Arg His Tyr Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa  
1 5 10 15

<210> 309  
<211> 15  
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<220>  
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<220>  
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<220>  
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<220>  
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<400> 309

Ala Ser Xaa Arg His Tyr Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa  
1 5 10 15

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<210> 310  
<211> 9  
<212> PRT  
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<220>  
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<220>  
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<223> bonded to OCH3

<220>  
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<223> N terminus is bonded to H

<400> 310

Ile Asn Pro Ile Tyr Arg Leu Arg Tyr  
1 5

<210> 311  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<223> Sequence is linked to identical sequence by a disulfide bond

<220>  
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<222> (1)..(1)  
<223> N terminus is bonded to H

<220>  
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<222> (9)..(9)  
<223> C terminus is bonded to NH2

<400> 311

Ile Asn Pro Cys Tyr Arg Leu Arg Tyr  
1 5

<210> 312  
<211> 6  
<212> PRT  
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<220>  
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<220>

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<222> (6)..(6)  
<223> C terminus is bonded to OCH3  
  
<220>  
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<223> sequence is linked to an identical sequence  
  
<220>  
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<222> (1)..(1)  
<223> N terminus is bonded to H  
  
<400> 312

Cys Tyr Arg Leu Arg Tyr  
1 5

<210> 313  
<211> 8  
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<222> (1)..(1)  
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<220>  
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<223> Connected by NH CH CO  
  
<220>  
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<222> (3)..(4)  
<223> Identical peptide chains are connected by (CH2)4 at the CH o  
f NH CH CO  
  
<400> 313

Ile Asn Pro Tyr Arg Leu Arg Tyr  
1 5

<210> 314  
<211> 10  
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<223> N terminus is bonded to H

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<220>  
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<223> C terminus is bonded to OCH3

<400> 314

Tyr Arg Leu Arg Tyr Tyr Arg Leu Arg Tyr  
1 5 10

<210> 315  
<211> 34  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<220>  
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<222> (18)..(22)  
<223>

<400> 315

Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp Met Ala  
1 5 10 15

Arg Cys Tyr Ser Ala Cys Arg His Tyr Ile Asn Leu Ile Thr Arg Gln  
20 25 30

Arg Tyr

<210> 316  
<211> 12  
<212> PRT  
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<220>  
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<400> 316

Arg His Tyr Leu Asn Leu Ile Gly Arg Gln Arg Tyr  
1 5 10

<210> 317  
<211> 12  
<212> PRT  
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<220>  
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<220>  
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<222> (3)..(7)  
<223> ACETYLATION

<400> 317



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Arg His Gly Leu Asn Leu Leu Gly Arg Gln Arg Tyr  
1 5 10

<210> 318  
<211> 10  
<212> PRT  
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<220>  
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<400> 318

Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr  
1 5 10

<210> 319  
<211> 11  
<212> PRT  
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<220>  
<223> Polypeptide variation

<400> 319

His Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr  
1 5 10

<210> 320  
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<220>  
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<400> 320

Arg His Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr  
1 5 10

<210> 321  
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<400> 321

Tyr Ile Asn Leu Leu Tyr Arg Gln Arg Tyr  
1 5 10

<210> 322  
<211> 15

4040.001000

<212> PRT

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<223> Polypeptide variation

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<221> MISC\_FEATURE

<222> (5)..(5)

<223> Xaa is 6 amino hexanoic acid

<400> 322

Tyr Pro Ser Leu Xaa Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr  
1 5 10 15

<210> 323

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

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<400> 323

Ile Asn Leu Ile Tyr Arg Leu Arg Tyr  
1 5

<210> 324

<211> 12

<212> PRT

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<223> N alpha ACETYLTATION

<220>

<221> MOD\_RES

<222> (12)..(12)

<223> AMIDATION

<400> 324

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10

<210> 325

<211> 15

<212> PRT

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<400> 325

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 326  
<211> 15  
<212> PRT  
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<223> N terminal is bonded to H

<220>  
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<222> (15)..(15)  
<223> AMIDATION

<400> 326

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 327  
<211> 9  
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<220>  
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<222> (9)..(9)  
<223> AMIDATION

<220>  
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<223> N alpha ACETYLATION

<400> 327

Ala Ser Leu Arg Thr Arg Gln Arg Tyr  
1 5

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<210> 328  
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<220>  
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<222> (6)..(6)  
<223> Xaa is 2 thienylalanine

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 328

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 329  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<223> N alpha ACETYLATION

<220>  
<221> MOD\_RES  
<222> (15)..(15)  
<223> AMIDATION

<400> 329

Tyr Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr  
1 5 10 15

<210> 330  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<400> 330

Asp Asp Asp Asp Tyr  
1 5

<210> 331  
<211> 3  
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Gly Pro Arg  
1

<210> 332  
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Ala Gly Gly  
1

<210> 333  
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<220>  
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<400> 333

His Pro Phe His Leu  
1 5

<210> 334  
<211> 34  
<212> PRT  
<213> Homo sapiens  
  
<400> 334

Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn  
1 5 10 15

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln  
20 25 30

Arg Tyr

4040.001000

<210> 335  
<211> 34  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide variation

<400> 335

Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp Met Ala  
1 5 10 15

Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln  
20 25 30

Arg Tyr

<210> 336  
<211> 37  
<212> PRT  
<213> Homo sapiens

<400> 336

His Asp Glu Phe Glu Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val  
1 5 10 15

Ser Ser Tyr Leu Glu Gly Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu  
20 25 30

Val Lys Gly Arg Gly  
35

<210> 337  
<211> 36  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> (36)..(36)  
<223> C terminus is bonded to NH2

<400> 337

His Asp Glu Phe Glu Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val  
1 5 10 15

Ser Ser Tyr Leu Glu Gly Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu  
20 25 30

Val Lys Gly Arg  
35

<210> 338  
<211> 31  
<212> PRT  
<213> Homo sapiens

4040.001000

<400> 338

His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly  
1 5 10 15

Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly  
20 25 30

<210> 339

<211> 30

<212> PRT

<213> Homo sapiens

<220>

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<222> (30)..(30)

<223> C terminus is bonded to NH2

<400> 339

His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly  
1 5 10 15

Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg  
20 25 30

<210> 340

<211> 37

<212> PRT

<213> Homo sapiens

<400> 340

His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Ser  
1 5 10 15

Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asp Thr Lys Arg Asn  
20 25 30

Lys Asn Asn Ile Ala  
35

<210> 341 <211> 463 <212> PRT <213> homo sapiens <400> 341

Met Ala Gly Ala Pro Gly Pro Leu Arg Leu Ala Leu Leu Leu Gly  
1 5 10 15

Met Val Gly Arg Ala Gly Pro Arg Pro Gln Gly Ala Thr Val Ser Leu  
20 25 30

Trp Glu Thr Val Gln Lys Trp Arg Glu Tyr Arg Arg Gln Cys Gln Arg  
35 40 45

Ser Leu Thr Glu Asp Pro Pro Pro Ala Thr Asp Leu Phe Cys Asn Arg  
50 55 60

4040.001000

Thr Phe Asp Glu Tyr Ala Cys Trp Pro Asp Gly Glu Pro Gly Ser Phe  
65 70 75 80

Val Asn Val Ser Cys Pro Trp Tyr Leu Pro Trp Ala Ser Ser Val Pro  
85 90 95

Gln Gly His Val Tyr Arg Phe Cys Thr Ala Glu Gly Leu Trp Leu Gln  
100 105 110

Lys Asp Asn Ser Ser Leu Pro Trp Arg Asp Leu Ser Glu Cys Glu Glu  
115 120 125

Ser Lys Arg Gly Glu Arg Ser Ser Pro Glu Glu Gln Leu Leu Phe Leu  
130 135 140

Tyr Ile Ile Tyr Thr Val Gly Tyr Ala Leu Ser Phe Ser Ala Leu Val  
145 150 155 160

Ile Ala Ser Ala Ile Leu Leu Gly Phe Arg His Leu His Cys Thr Arg  
165 170 175

Asn Tyr Ile His Leu Asn Leu Phe Ala Ser Phe Ile Leu Arg Ala Leu  
180 185 190

Ser Val Phe Ile Lys Asp Ala Ala Leu Lys Trp Met Tyr Ser Thr Ala  
195 200 205

Ala Gln Gln His Gln Trp Asp Gly Leu Leu Ser Tyr Gln Asp Ser Leu  
210 215 220

Ser Cys Arg Leu Val Phe Leu Leu Met Gln Tyr Cys Val Ala Ala Asn  
225 230 235 240

Tyr Tyr Trp Leu Leu Val Glu Gly Val Tyr Leu Tyr Thr Leu Leu Ala  
245 250 255

Phe Ser Val Phe Ser Glu Gln Trp Ile Phe Arg Leu Tyr Val Ser Ile  
260 265 270

Gly Trp Gly Val Pro Leu Leu Phe Val Val Pro Trp Gly Ile Val Lys  
275 280 285

Tyr Leu Tyr Glu Asp Glu Gly Cys Trp Thr Arg Asn Ser Asn Met Asn  
290 295 300

Tyr Trp Leu Ile Ile Arg Leu Pro Ile Leu Phe Ala Ile Gly Val Asn  
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4040.001000  
315

305

310

320

Phe Leu Ile Phe Val Arg Val Ile Cys Ile Val Val Ser Lys Leu Lys  
325 330 335

Ala Asn Leu Met Cys Lys Thr Asp Ile Lys Cys Arg Leu Ala Lys Ser  
340 345 350

Thr Leu Thr Leu Ile Pro Leu Leu Gly Thr His Glu Val Ile Phe Ala  
355 360 365

Phe Val Met Asp Glu His Ala Arg Gly Thr Leu Arg Phe Ile Lys Leu  
370 375 380

Phe Thr Glu Leu Ser Phe Thr Ser Phe Gln Gly Leu Met Val Ala Ile  
385 390 395 400

Leu Tyr Cys Phe Val Asn Asn Glu Val Gln Leu Glu Phe Arg Lys Ser  
405 410 415

Trp Glu Arg Trp Arg Leu Glu His Leu His Ile Gln Arg Asp Ser Ser  
420 425 430

Met Lys Pro Leu Lys Cys Pro Thr Ser Ser Leu Ser Ser Gly Ala Thr  
435 440 445

Ala Gly Ser Ser Met Tyr Thr Ala Thr Cys Gln Ala Ser Cys Ser  
450 455 460